International Journal of Reproductive BioMedicine
Volume 19, Issue no. 1, https://doi.org/10.18502/ijrm.v19i1.8177
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Research Article

# Underexpression of *hsa-miR-449* family and their promoter hypermethylation in infertile men: A case-control study

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Received 5 September 2019
Revised 12 January 2020
Accepted 9 June 2020

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Editor-in-Chief:
Aflatoonian Abbas M.D.

## Abstract

**Background:** Post-transcriptional microRNAs (miRNAs) have a impotrant pattern in the spermatogenesis process.

**Objective:** Study of the expression and methylation of *hsa-miR-449* family in sperm samples of infertile men.

**Materials and Methods:** In this case-control study, we recruited 74 infertile men (with asthenozoospermia, teratozoospermia, asthenoteratozoospermia, and oligoasthenoteratozoospermia) and 30 control samles. Methylation-specific PCR (MSP) method was used for methylation evaluation of *hsa-miR-449 a, b, c* promoter. By Real time PCR (qRT-PCR) method,we showed downregulation of *hsa-miR-449 a, b, c* in the sperm samples of infertile men and compared it to their fertile counterparts.

**Results:** There was significant underexperssion, in *hsa-miR-449-b* in oligoasthenoteratospermic samples ($p = 0.0001$, $F = 2.9$). About the methylation pattern, infertile men showed high frequency of methylation in the promoter of *hsa-miR-449 a, b, c* in comparison to controls (60.8% vs 23.3%), the highest amount of methylation was observed in oligoasthenoteratospermia samples (81.2%).

**Conclusion:** In this study, low expression and high methylation of *hsa-miR-449-b* were observed in infertile men in compared to control samples, which can be one of the causes of defective spermatogenesis.

***Key words:*** *Spermatogenesis, miR-449, Expression, Epigenetic.*

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